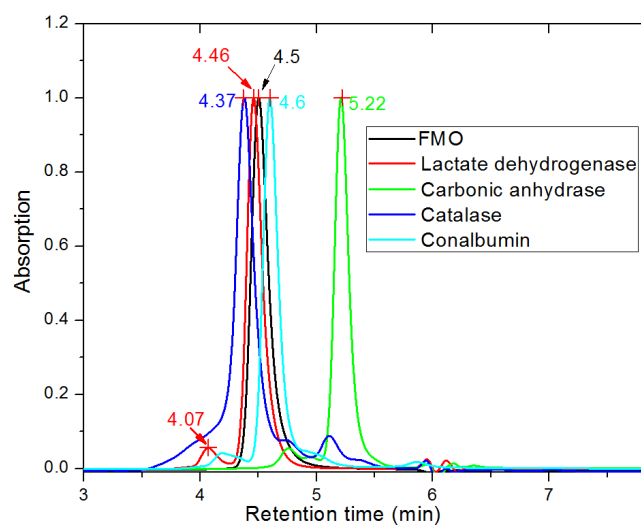


Supplemental information

Structural model and spectroscopic characteristics of the FMO antenna protein from the aerobic chlorophototroph, *Candidatus Chloracidobacterium thermophilum*

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Bryant³, Robert E. Blankenship^{1,2*}



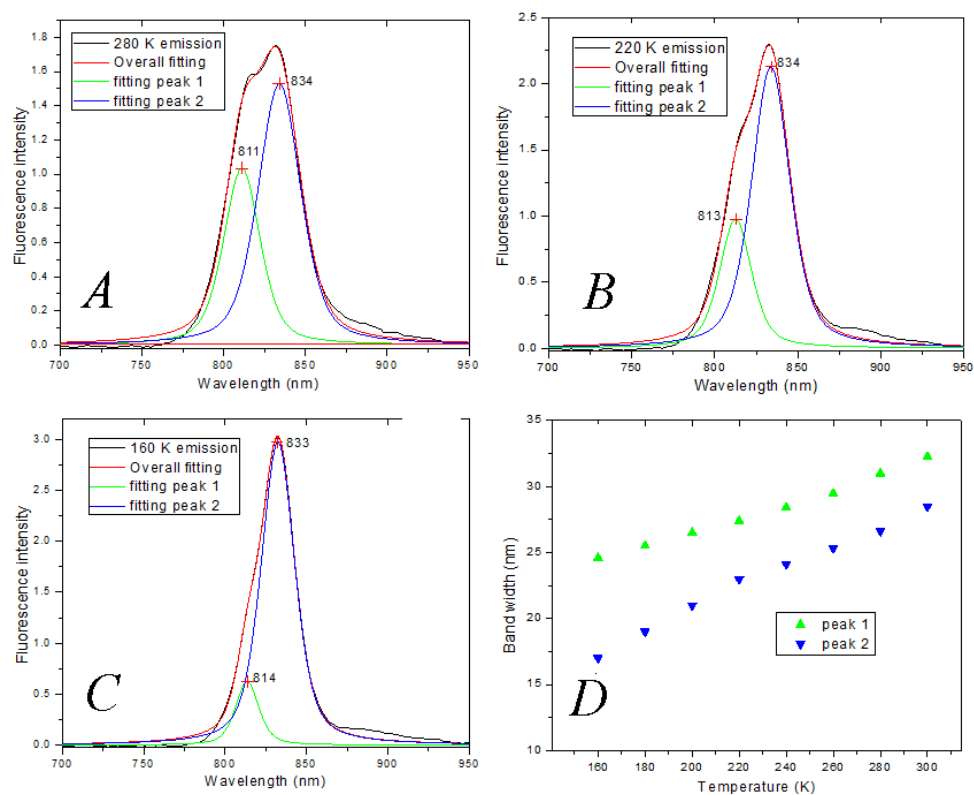
SI Fig. 1 Elution profiles of *C. thermophilum* FMO and protein standards from the analytical gel filtration column.

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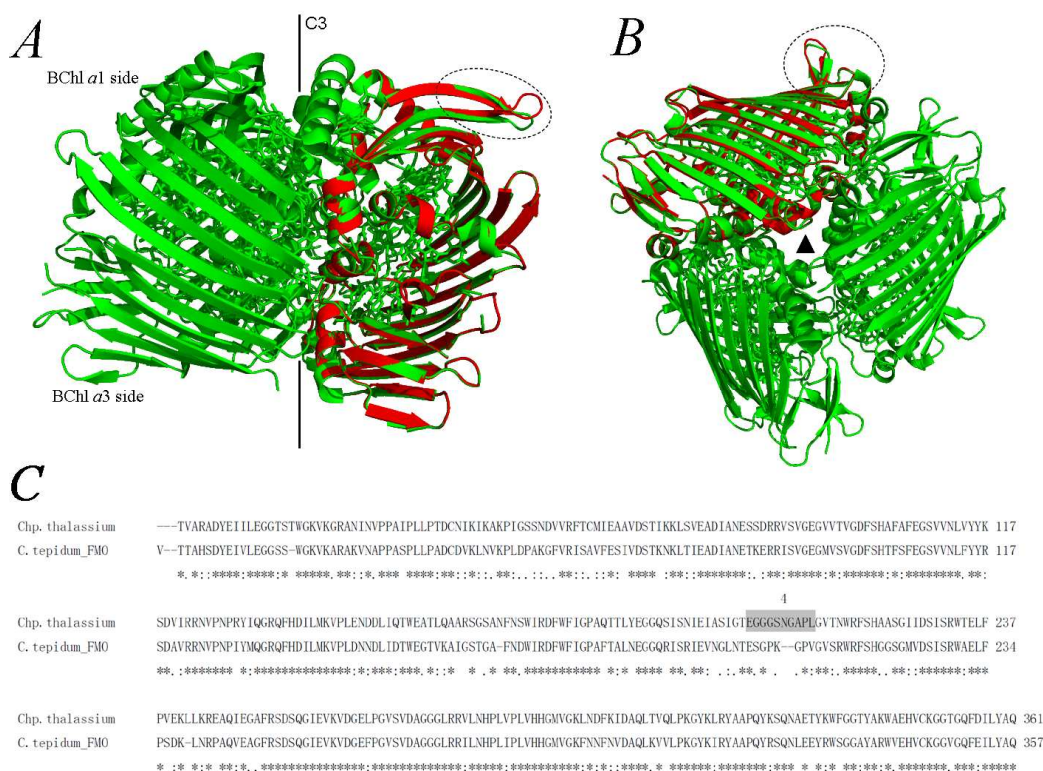
C.thermophilum_FMO      ---SKLTTSNYDLDDL1A--TCWGTLRAEARISNVPSASPLPIDGELKLEAKKI2E--DDV 53
C.tepidum_FMO           D-VTTAASHDYIEVLVEGGSSSGWKVKARAKV-NAPPASPLLPADCDVKLVNKPDPKAGF 57
                        * : **** : * : **** : * : **** : * : **** : * : ..
C.thermophilum_FMO      VRLTFFGQSIVDGILGRVEGESDIANESPTRRVAAGDGKITVGKFSHRFEFEGVVDCLRY 113
C.tepidum_FMO           VRISAVFESISVDSTKNKLTIEDIANETKERRISVGEGMVSVDGSHTFSFEGSVVNLFY 117
                        *** : . : **** : . : * : ***** : * : ** : * : * : * : *
                                3
C.thermophilum_FMO      WRSKAIDDN3LIAKKQRLLCGNLFDHLSVRVPLDSEEVIDTWLEMQDAFRNSPNEFGDIKD 173
C.tepidum_FMO           YRSDAVARRNV--FNPIYMQRQFHDILMKVFLDNNDLIDTWEGTVKAIGSTGAENDWIRD 175
                        *** : * : * : * : * : * : * : * : * : * : * : * : * : *
                                4
C.thermophilum_FMO      VWLIGLPLWNALEQTGQSLDN4IDVYYFSEVEGECKSRID---FFFAGGGTGIVDSISRWL 230
C.tepidum_FMO           FWFIFGPAFTALNEGQGISRIEVENGLN-TESGPKGPVGVSRWRFSHGSGMVDSISRWAE 234
                        . : *** : * : * : * : * : * : . : . * : * : . : . : * : * : * : * : *
                                5
C.thermophilum_FMO      LFPIDGLG5KPVNQGGRVARLQGNNFNASVQGI EVKLFVELPGFSVPFIEGGRKVLNHPLVP 290
C.tepidum_FMO           LFPSDKLNRP-----AQVEAGFRSDSQGIEVKVDGEFFPGVSVDAGGGLRRILNHPLIP 287
                        *** * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
                                6
C.thermophilum_FMO      LAHHGI AVNSEPADLAIRFKVSI PKKKFIETANSF EWDR6VAENV6VFTGGRYKAWAEGI 350
C.tepidum_FMO           LVHHGMVGKFNNFNVDQAQLKVLPKGYKIRYAAPQYRSQNLEE--YRWSGGAYARWEHV 345
                        * . *** : . : : : : : * : * : * : * : * : * : * : * : * : * :
C.thermophilum_FMO      CKGSYSYPFDIFFG- 363
C.tepidum_FMO           CKGGVGQFEILY AQ 359
                        *** * : * : * : * : * : * : * : * : * : * : * : * :

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SI Fig. 2 Sequence alignment of the FMO protein from *Chlorobaculum tepdium* (C.tepdium_FMO) and *Candidatus* Chloroacidobacterium thermophilum (C.thermophilum_FMO) used for structure homology modeling. Six sequence insertion or deletion regions are labeled sequentially from 1 to 6, which show structural differences on the C. thermophilum FMO in comparison to FMO structure from *C. tepdium*.



SI Fig. 3 The fluorescence emission spectra of *C. thermophilum* FMO at 280 (A), 220 (B) and 160 K (C) were deconvoluted by two Gaussian-Lorentzian Sum function using PeakFit. The widths of the two deconvoluted peaks are plotted against the temperature in panel (D). A linear relationship between the peak widths and temperature exhibited.



SI Fig. 4 Homology structural modeling of the FMO protein from *Chp. thalassium*, which is the distantly related form of FMO in GSB. (A) Side view of the FMO trimer. (B) View of the FMO trimer from the BChl a_3 side. Homology structure of the *Chp. thalassium* FMO protein (red) shows much more structural similarity to the FMO from *C. tepidum* (green) except the CsmA binding region, which is circled. The CsmA from *Chp. thalassium* is also quite divergent from the other CsmAs of GSB (main text). (C) Sequence alignment of FMOs from *Chp. thalassium* and *C. tepidum*. The structurally different region is highlighted and corresponding to region 4.